

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on:

May 15, 2002, 07:57:59 ; Search time 33.64 Seconds

(without alignments)

1397.311 Million cell. updates/sec

Title: score: US-09-783-320-4

Perfect score: 624.3

Sequence: MEKVYVRLQKIGESESGFRAIL.....YAKILHIVMADGAYQEDNDE 1214

Scoring table: BLOSUM62  
Gapopen 10.0 , Gapext 0.5  
Searched: 10524 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3385	54.2	774	1 NEKL_MOUSE
2	817.5	13.6	841	1 NEKL_HUMAN
3	833	13.3	511	1 NEK3_MOUSE
4	790.5	10.7	459	1 NEK3_HUMAN
5	565.5	9.1	439	1 NEKL_TRYR
6	550	8.8	445	1 NEK2_HUMAN
7	540.5	8.7	443	1 NEK2_MOUSE
8	530.5	8.5	599	1 NIMA_EMENT
9	528.5	8.5	431	1 NIMA_TRYR
10	503.5	8.0	1142	1 GIN4_YEAST
11	499.5	7.5	779	1 NIMI_NECCR
12	468.5	7.5	966	1 ST10_MOUSE
13	455	7.3	968	1 ST10_HUMAN
14	452	7.2	1518	1 KKL1_YEAST
15	437.5	7.0	1 KCC4_YEAST	
16	435	6.9	1 KIN3_YEAST	
17	421.5	6.8	1 KIK3_CHEC1	
18	393	6.3	1 KIK1_YEAST	
19	368	6.2	1062	1 CCK7_SHCPO
20	383.5	6.1	705	1 CCK7_YEAST
21	382.5	6.1	740	1 KKL1_HUMAN
22	382	6.1	713	1 KKL1_HUMAN
23	381	6.1	460	1 CDS1_SHCPO
24	380.5	6.1	685	1 SIR_HUMAN
25	380	6.1	682	1 SIRK_RAT
26	379	6.1	682	1 SIRK_MOUSE
27	378	6.1	631	1 CIRK_MOUSE
28	378	6.1	733	1 K6A1_HUMAN
29	378	6.1	733	1 K6A2_MOUSE
30	378	6.1	735	1 K6A1_HUMAN
31	378	6.1	735	1 K6A1_RAT
32	377.5	6.0	733	1 K6A1_XENLA
33	377.5	6.0	1 GAK_RAT	
1305				

### ALIGNMENTS

RESULT 1  
NEKL\_MOUSE STANDARD; PRT: 774 AA.  
ID NEKL\_MOUSE  
AC P51954;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
RN 11  
PP SEQUENCE FROM N.A.  
RC TISSUE-BLOOD;  
RX MEDLINE-3301942; PUBMED-1382974;  
RA Letwin K., Mizzen L., Motro B., Ben-David Y., Bernstein A.,  
RA Pawson T.;  
RT "A mammalian dual specificity protein kinase, Nek1, is related to the  
RT NIMA cell cycle regulator and highly expressed in meiotic germ  
RT cells";  
RL ENBO J. 11:3521-3531(1992).  
CC 1- FUNCTION: PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS  
TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF  
MITOSIS.  
CC 2- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).  
CC 3- TISSUE SPECIALITY: PREDOMINANTLY IN TESTIS (GERM CELLS AND  
SEROTYL CELLS), LOWER LIVER, OVARY (OVOCYTES AND GRANULOSA  
CELLS), THYMUS, AND LUNG.  
CC 4- DEVELOPMENTAL STAGE: IN FEMALE, EXPRESSED AS POLYCIES ENTER THE  
SECONDARY STAGE UNTIL OVULATION OCCURS. IN THE MALE REPRODUCTIVE  
SYSTEM, THE EXPRESSION IS LIMITED TO SPERMATOCTES AND SPERMATIDS.  
CC 5- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC 6- NIMA SUBFAMILY.  
CC 7- This SWISS-PROT entry is copyright. It is produced through a collaboration  
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DR EMBL: S45028; AAB33529; 1; -  
DR HSSEB; 2P941; 1B9;  
DR MGDB; MGI:197301; NEKL;  
DR InterPro; IPR00719; Euk-ppk kinase;  
DR InterPro; IPR00230; Ser-thr-ppk kinase;  
DR SMART; SM00230; S\_TK\_C1;  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1;  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1;  
DR PROSITE; PS5011; PROTEIN\_KINASE\_DOM; 1;  
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;

KW	Nuclear protein; Phosphorylation; Cell cycle; Cell division;	DE	Serine/threonine protein kinase 2 (EC 2.7.1.37) (serine/threonine-
TYROLINE-PROTEIN KINASE.	PROTEIN KINASE.	protein kinase NRK2).	
FT DOMAIN 4 258	ATP (BY SIMILARITY).	STK2.	
FT NP-BIND 10 18	ATP (BY SIMILARITY).	Homosapiens (Human).	GN
FT BIND 33 33	ATP (BY SIMILARITY).	Chordata; Craniata; Vertebrata; Euteleostomi;	OS
FT ACT-SITE 128 128	BY SIMILARITY.	Mammalia; Eutheria; Primates; Catarhini; Homo.	OC
SEQUENCE 774 AA: 88427 MM: 7EDE5B1ACCC06FA CRC64;		NBLToxid-9506;	OX
RR [1]			
Query Match 54.2%; Score 3305; DB 1; Length 774;		SEQUENCE FROM N. A.	
Best Local Similarity 85.5%; Pred. No. 1.2e-118;		TISSUE-Breast;	
Matches 665; Conservative 45; Mismatches 64; Indels 4; Gaps 3;		RX	
QY 1 MEKYVLRQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 60	NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	Medline; 91268133; Published=810854;	
Db 1 MEKYVLRQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 60	181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	RA	
QY 61 PNTIVQKSEEEFNGSLIVMDYCEGSDLFRINQGALFQDQDIDMPOVIAALKH 120	121 DRKJLARDKSONFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 180	RA	
Db 61 PNTIVQKSEEEFNGSLIVMDYCEGSDLFRINQGALFQDQDIDMPOVIAALKH 120	121 DRKJLARDKSONFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 180	RA	
QY 121 DRKJLARDKSONFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 180	121 DRKJLARDKSONFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 180	RA	
Db 121 DRKJLARDKSONFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 180	181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	RA	
QY 181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	RA	
Db 181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	181 NNKSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 240	RA	
QY 241 RNPDRPSPNSISLKGFTAKRTEKEFSPOLAEFCFLTSKGPPPLGKPPGQGVS 300	301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	RA	
Db 241 RNPDRPSPNSISLKGFTAKRTEKEFSPOLAEFCFLTSKGPPPLGKPPGQGVS 300	301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	RA	
QY 301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	RA	
Db 301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	301 SFVPAQKIKPAPKYGFLPTKTYKGKKLKKPPKPKQHAIPIYKMSGEENKME 360	RA	
QY 361 EAKRKRLFETEKKORDQIISLMRABKQKQERERLIRINHAREGQWNRVNLASGGSE 420	361 EAKRKRLFETEKKORDQIISLMRABKQKQERERLIRINHAREGQWNRVNLASGGSE 420	RA	
Db 361 EAKRKRLFETEKKORDQIISLMRABKQKQERERLIRINHAREGQWNRVNLASGGSE 420	361 EAKRKRLFETEKKORDQIISLMRABKQKQERERLIRINHAREGQWNRVNLASGGSE 420	RA	
QY 421 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	420 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	RA	
Db 420 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	420 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	RA	
QY 480 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	480 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	RA	
Db 480 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	480 VKAPELGSCTIAPSSSSRQGOYHKAITPOMOORADENAEKWKEIETGGLPERQG 480	RA	
QY 541 EAHNSGEGOGRSEADMRKPKISLKAHANARAAVKEEOLERKEKEAEREKPYHEHVA 600	481 GLAVERAKOBEFQKREMKARAGHIVYLARLQIRQNLQNRQKAKRGERK 540	RA	
Db 541 EAHNSGEGOGRSEADMRKPKISLKAHANARAAVKEEOLERKEKEAEREKPYHEHVA 600	481 GLAVERAKOBEFQKREMKARAGHIVYLARLQIRQNLQNRQKAKRGERK 540	RA	
QY 540 EADGTTGQBTSTEEDWRLKMKMESLAKIKAQINARAVAKQERERKREKRVWHEHLA 599	480 VLAVERAKOBEFQKREMKARAGHIVYLARLQIRQNLQNRQKAKRGERK 540	RA	
Db 540 EADGTTGQBTSTEEDWRLKMKMESLAKIKAQINARAVAKQERERKREKRVWHEHLA 599	480 VLAVERAKOBEFQKREMKARAGHIVYLARLQIRQNLQNRQKAKRGERK 540	RA	
RESULT 2	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
STK2_HUMAN	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
ID STK2_HUMAN	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
STK2_HUMAN	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
P51957;	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
DT 01-OCT-1996 (rel. 34, Last sequence update)	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
DT 16-OCT-2001 (rel. 40, Last annotation update)	501 KQVKSDDVSPPLGQHETGGPSKQHRSVSVTSALKAVGVDVSLTDRETESEMOKTN 650	RA	
Db 657 AIISSKEILRLRNENLKAQEDKGMDLSPFEINHEADEKEKEKVSSEDRKWEAG 720	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
Db 657 AIISSKEILRLRNENLKAQEDKGMDLSPFEINHEADEKEKEKVSSEDRKWEAG 720	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
QY 721 QLVIPDAVLTDSRPSATEKHTVGEVILKLDNSGSPKRVKGNPDSVLUKIGEABLQ 774	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
Db 717 QLVIPDAVLTDSRPSATEKHTVGEVILKLDNSGSPKRVKGNPDSVLUKIGEABLQ 774	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
QY 774 AA: 88427 MM: 7EDE5B1ACCC06FA CRC64;	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
Db 774 AA: 88427 MM: 7EDE5B1ACCC06FA CRC64;	6 YKLQLQKIGESFGKALIVKSTEDGROVKVKEINISMSSKERSREVAVLNKKH 63	RA	
QY 123 KILRKDQSLQFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 182	123 KILRKDQSLQFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 182	RA	
Db 123 KILRKDQSLQFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 182	123 KILRKDQSLQFLRKGTVGVLQDFGFLARVLNSTPLARTCTGTPYIISPECEENPY 182	RA	
QY 183 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	183 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	RA	
Db 183 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	183 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	RA	
QY 186 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	186 KSDIWAQCVYELCTKIAFEAGSMKNUVLTISCFPPVLSYDLSVSLPK 242	RA	